

SEQUENCE LISTING

<110> Duvick, Jonathan P.
Gilliam, Jacob T.
Maddox, Joyce R.
Rao, Aragula Gururaj
Crasta, Oswald R.
Folkerzts, Otto

<120> Amino Polyol Amine Oxidase
Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<150> US 60/092,936
<151> 1998-07-25

<150> US 60/135,391
<151> 1999-05-21

<150> US 09/352,159
<151> 1999-07-12

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tgctatagta	gcccaggata	gaattttccg	ccaatgcttg	gtcccatata	300
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gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt Glu Ala Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser Gly 35 40 45	144
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tcc aat gac Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp 50 55 60	192
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu 65 70 75 80	240
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288

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gtt cca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc															384			
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile			
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gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg															432			
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gcc ggc ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg															816			
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu			
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tat ccc acc ttg aca ttt tca cca cct ctt ccc gca gag aag caa gca															864			
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala			
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Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val			
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gat	cga	caa	tgg	tcc	att	acc	tgt	tcc	atg	gtc	gga	gac	ccg	gga	cg	1056		
Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg			
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aag	tgg	tcc	caa	cag	tcc	aag	cag	gt	caa	aag	tct	gtc	tgg	gac	1104			
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Ser	Val	Trp	Asp				
355															360	365		
caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	gg	gcc	caa	gtc	cca	gag	ccg	1152		
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro			
370															375	380		
gcc	aac	gig	ctc	gaa	atc	gag	tgg	tcc	aag	cag	cag	tat	tcc	caa	gga	1200		
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly			
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gtc	ccg	agc	gcc	gtc	tat	gg	ctg	aac	gat	ctc	atc	aca	ctg	gg	tcc	1248		
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser			
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ccg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	tcc	gtt	gga	acg	gag	acg	1296		
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr			
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tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcc	gg	caa	1344		
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln			
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ccg	gg	gt	gc	ga	gg	gt	gt	gc	gg	cc	ga	cc	gca	cc	gca	1386		
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Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly			
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Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp			
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Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Ieu	Glu			
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Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp			
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Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu		
145	150	155
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly		
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys		
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Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly		
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Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met		
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Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala		
225	230	235
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly		
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Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu		
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Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala		
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Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val		
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Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln		
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Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val		
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Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg		
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Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro		
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Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly		
385	390	395
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser		
405	410	415
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr		
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Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	
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gag	gog	atg	cat	cgt	gtt	ggg	gga	aag	act	ctg	agc	gtt	caa	tcc	ggt	144
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	
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ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gog	tgg	atc	aat	gac	192
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	
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ggc	gag	cic	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	283
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	
85				90						95						

ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	336
Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu		
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gtt	gca	agt	gca	ctt	gct	gaa	ctc	ctc	ccc	gtt	tgg	tct	cag	ctg	atc	384
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	
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gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gct	agc	cct	cag	gct	aag	cg	432
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	
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ctc	gac	agt	gtg	agc	tcc	gct	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Leu	Asn	Leu		
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Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Gly		
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gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ctc	acc	gac	tac	atc	aag	576
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
180				185					190						

agt	gcc	acc	ggt	ctc	agt	aat	att	tcc	tgc	gac	aag	aaa	gac	ggc	gg	624
Ser	Ala	Thr	Gly	Ile	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	
195				200					205							

cag	tat	gtg	cga	tgc	aaa	aca	g	gtgcgtgtgg	tgtcgccctca	gggtggggggac	-----	676			
Gln	Tyr	Val	Arg	Cys	Lys	Thr									

210

215

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att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala 245 250 255	824
gtg tcc cga aac aag gtg gtg gtt tcg tta ccc aca acc ttg tat Val Phe Arg Ser Lys Val Val Ser Leu Pro Thr Thr Leu Tyr 260 265 270	872
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 275 280 285	920
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp 290 295 300 305	968
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cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccc gga cgg aag Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys 340 345 350	1112
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ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccc gcc Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala 370 375 380 385	1208
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ctc aga acg ccc ttc aag agt gtt cat ttc gtt gga acg gag acg tct Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser 420 425 430	1352

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 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Ile Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
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 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
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 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg

340	345	350	
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Gln Ieu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro			
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Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly			
385	390	395	400
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser			
405	410	415	
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr			
420	425	430	
Ser Ieu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln			
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Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly			
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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
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Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu			
65	70	75	80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
85	90	95	
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100	105	110	
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
115	120	125	
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
130	135	140	
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
145	150	155	160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly			
165	170	175	
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys			
180	185	190	
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
195	200	205	
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly			
210	215	220	
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met			
225	230	235	240
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro			
245	250	255	
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro			
260	265	270	
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln			
275	280	285	

<210> 10
<211> 1392
<212> DNA
<213> *Exophiala spinifera*

<220>
<221> CDS
<222> (1) ... (1389)

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<221> misc_feature
<222> (1)...(3)
<223> Extra lysine in K:trAPAO
```

<400> 10

aaa gac aac gtt gcg gac gtc gta gtg gtg ggc gct ggc ttg agc ggt
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt		
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val		
20	25	30

cit gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg
 Ieu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

```

ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
      50           55           60

```

```

gac agc aac caa agc gaa gta tcc aca ttg ttt gaa aga ttt cat ttg
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65          70          75          80

```

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
10

Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln		
85																95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag															336		
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu			
100															110		
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg															384		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu		
115															125		
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag															432		
Ile	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys			
130															140		
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac															480		
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn		
145															155		
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc															528		
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu		
165															175		
ggg gaa gac gac gag atc agc atg ctt ttt ctc acc gac tac atc															576		
Gly	Val	Glu	Ala	His	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile			
180															190		
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc															624		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly		
195															205		
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc															572		
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala		
210															220		
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc															720		
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
225															235		
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg															768		
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser		
245															255		
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc															816		
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr		
260															270		
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa															864		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln		
275															285		
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc															912		
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe		
290															300		
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc															960		
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		

305	310	315	320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335				1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350				1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365				1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380				1152
ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400				1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggi Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415				1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Iys Ser Val His Phe Val Gly Thr Glu 420 425 430				1296
acg tct tta gtt tgg aaa ggg tat aag gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445				1344
caa cga ggt gct gca gaa gtt gtg gct aac ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450 455 460				1389
tag				1392
<pre> <210> 11 <211> 463 <212> PRT <213> Exophiala spinifera </pre>				
<pre> <400> 11 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly 1 5 10 15 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val 20 25 30 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95 </pre>				
12				

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into
expression vectors, N23256

<400> 12

ggggaaattca aagacaacgt tgccggacgtg gtag 34

<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into expression vectors, N23259

<400> 13
 ggggcggccg cctatgtgc tggcaccagg ctag 34

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
 tggtttcgtt accgacaacc ttgtatccc 29

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15
 gagttggtcc cagacagact ttgtcgt 28

<210> 16
 <211> 1673
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> sig_peptide
 <222> (1)...(267)
 <223> yeast alpha mating factor secretion signal.

<221> CDS
 <222> (1)...(1662)

<400> 16
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 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 95
 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
 -70 -65 -60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe -55 -50 -45	144
gat gtt gct gtt ttt cca ttt tcc aac agc aca aat aac ggg tta ttg Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -40 -35 -30	152
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val -25 -20 -15 -10	240
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala -5 1 5	288
gac ggg gta ttg ttg ggc gct ggc ttg aac ggt ttg gag acg gca cgc Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 10 15 20	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 25 30 35	384
cgt gta ggg gga aag act ctg agc gta caa tcc ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 40 45 50 55	432
atc atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 60 65 70	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 75 80 85	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 90 95 100	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Val Ala Ser Ala 105 110 115	624
ctt gcg gaa ctc ctc ccc gta ttg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 120 125 130 135	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Glu Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 150	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 155 160 165	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac 15	816

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His			
170	175	180	
gag acc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt			364
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly			
185	190	195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga			912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg			
200	205	210	215
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt			960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu			
220	225	230	
gtt cca ggc tca gtg cac ctc zac acc ccc gtc gct gaa att gag cag			1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Cln			
235	240	245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga			1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			
250	255	260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg			1104
Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			
265	270	275	
aca ttt tca cca ccc ctt ccc gcc gag aag caa gca ttg gct gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
280	285	290	295
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
300	305	310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
315	320	325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
330	335	340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
345	350	355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
360	365	370	375
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
380	385	390	
caa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Glu Gly Ala Pro Ser Ala			
395	400	405	

gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg 1536
 Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
 410 415 420

ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg 1584
 Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
 425 430 435

aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca 1632
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
 440 445 450 455

gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c 1673
 Glu Val Val Ala Ser Leu Val Pro Ala Ala
 460 465

<210> 17
 <211> 554
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> SIGNAL
 <222> (1)...(89)

<400> 17
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
 -70 -65 -60
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 -55 -50 -45
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -40 -35 -30
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -25 -20 -15 -10
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 -5 1 5
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
 10 15 20
 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
 25 30 35
 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
 40 45 50 55
 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
 60 65 70
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
 75 80 85
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
 90 95 100
 Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
 105 110 115
 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
 120 125 130 135
 Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
 140 145 150

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
 155 160 165
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
 170 175 180
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
 185 190 195
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
 200 205 210 215
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
 220 225 230
 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
 235 240 245
 Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
 250 255 260
 Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
 265 270 275
 Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
 280 285 290 295
 Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
 300 305 310
 Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
 315 320 325
 Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
 330 335 340
 Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
 345 350 355
 Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
 360 365 370 375
 Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
 380 385 390
 Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
 395 400 405
 Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
 410 415 420
 Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
 425 430 435
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
 440 445 450 455
 Glu Val Val Ala Ser Leu Val Pro Ala Ala
 460 465

<210> 18

<211> 2079

<212> DNA

<213> Unknown

<220>

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
 - 687, gst fusion + polylinker, 688-2076,
 K:trAPAO, extra lysine underlined; 2077-2079, stop
 codon. For bacterial expression.

<221> CDS

<222> (1)...(2076)

<221> misc_feature

<222> (1)...(687)

<223> gst fusion + polylinker

<221> misc_feature

<222> (688)...(2076)

<223> K:trAPAO

<221> misc_feature

<222> (688)...(690)

<223> Extra lysine

<400> 18

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Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
1				5					10					15	

48

act	cga	cct	ctt	ttg	gaa	tat	ctt	gaa	aaa	tat	gaa	gag	cat	ttg
Thr	Arg	Ieu	Ieu	Glu	Tyr	Leu	Glu	Glu		Tyr	Glu	Glu	His	Ieu
20				25						30				

96

tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
35				40					45						

144

ggt	ttg	gag	ttt	ccc	aaa	ctt	cct	tat	tat	att	gat	ggt	gat	gtt	aaa
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
50				55					60						

192

ata	aca	cag	tct	atg	gcc	att	cc	ata	cgt	tat	ata	gct	gac	aag	cac	aac
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65				70					75			80				

240

atg	ttg	ggt	ttt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ttt	gaa
Met	Leu	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
85				90					95					

288

gga	gcg	gtt	ttg	gat	att	aga	tac	ggt	gtt	tcg	aga	att	gca	tat	agt
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
100				105					110						

336

aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	aag	cta	cct	gaa
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
115				120					125						

384

atg	ctg	aaa	atg	tcc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
130			135						140						

432

ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145			150						155			160			

480

gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	cta
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Ieu	Asp	Ala	Phe	Pro	Lys	Leu
165			170						175						

528

gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac
Val	Cys	Phe	Lys	Lys	Arg	Ile	Gl	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
180			185						190						

576

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gga tcc ccc gaa ttc aac gac aac gtt gcg gac gtg gta ttg gtc ggc Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Gly 225 230 235 240	720
gct cgc ttg agc ggt ttg gag acg gca cgc aac gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 245 250 255	758
cgg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Lys Thr 260 265 270	816
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285	864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300	912
gaa aga tt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305 310 315 320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp 325 330 335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340 345 350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag ggc Val Trp Ser Gln Leu Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355 360 365	1104
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gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385 390 395 400	1200
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ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg 20	1296

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Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln		
435	440	445
tgc att tgc cat gcc atg tca aag gaa ctt gtc cca ggc tca gtg cac		1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His		
450	455	460
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Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr		
465	470	475
gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt		1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val		
485	490	495
tgc tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt		1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu		
500	505	510
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Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr		
515	520	525
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc		1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Arg Glu Gln Gly		
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tcc tcc ggc gtc ctc caa tcc agc tgt gac ccc atc tca ttt gcc aga		1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg		
545	550	555
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg		1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met		
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gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga		1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg		
580	585	590
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Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly		
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gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcc aag		1872
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Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp		
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ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc aag agt gtt cat		1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His		
645	650	655

ttc gtt gga acg gag acg tct tta gtc tgg aaa ggg tat atg gaa ggg Phe Val Gly Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly 660 665 670	2016																																																																												
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu 675 680 685	2064																																																																												
gtg cca gca gca tag Val Pro Ala Ala 690	2079																																																																												
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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro																																																																													
1 5 10 15																																																																													
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu																																																																													
20 25 30																																																																													
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu																																																																													
35 40 45																																																																													
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys																																																																													
50 55 60																																																																													
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn																																																																													
65 70 75 80																																																																													
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu																																																																													
85 90 95																																																																													
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser																																																																													
100 105 110																																																																													
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu																																																																													
115 120 125																																																																													
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn																																																																													
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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp																																																																													
145 150 155 160																																																																													
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu																																																																													
165 170 175																																																																													
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr																																																																													
180 185 190																																																																													
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala																																																																													
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Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg																																																																													
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225 230 235 240																																																																													
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly																																																																													
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Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr																																																																													
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290 295 300																																																																													

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
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 340 345 350
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 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495
 Ser Leu Pro Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525
 Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
 580 585 590
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
 595 600 605
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
 610 615 620
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 625 630 635 640
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 645 650 655
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
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 Val Pro Ala Ala
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<220>
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fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464 , trAPAO cDNA.

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<223> Barley alpha amylase signal sequence

<221> misc_feature
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<221> CDS
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<223> Added lysine residue

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48

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96

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144

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192

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240

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288

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Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
75 80 85

336

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Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro
90 95 100

384

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Tyr Gly Asp Ser Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
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432

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aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtc gaa atc gag Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu 380 385 390	1248
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly 395 400 405	1296
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys 410 415 420	1344
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Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly 25 30 35 40	
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn 45 50 55	
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Ser	Glu	Glu
Val	Ala	Ser
Leu	Ala	Leu
Ala	Glu	
105	110	115
Leu	Leu	Pro
Pro	Val	Trp
Ser	Gln	Ser
Leu	Ile	Glu
Ile	Glu	His
Glu	His	Ser
His	Ser	Leu
Gln	Gln	Asp
Leu	Asp	Ser
Lys	Arg	Val
Ala	Leu	Ser
Ser	Pro	Val
Pro	Gln	Asp
Gln	Ala	Ser
Ala	Lys	Phe
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Ala	Ser	Pro
Pro	Gln	Ala
Gln	Ala	Lys
Ala	Lys	Arg
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Leu	Asp	Ser
Asp	Ser	Val
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Leu	Asn	Leu
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Pro	Ala	Val
Ala	Val	Leu
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Thr	Arg	Ala
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Leu	Gly	Val
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Ala	His	Glu
His	Ile	Ser
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Met	Leu	Phe
Leu	Thr	Asp
Thr	Tyr	Ile
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Thr	Gly	Leu
Leu	Ser	Asn
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185	190	195
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Met	Arg	Cys
Cys	Lys	Thr
Thr	205	210
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Gln	Ser	Ile
Ile	Cys	His
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Met	Ser	Lys
Lys	Glu	Leu
Leu	Val	Pro
Pro	Gly	
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His	Leu	Asn
Asn	Thr	Pro
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Ile	Glu	Gln
Gln	Ser	Ala
Ala	235	240
235	240	245
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Thr	Val	Arg
Arg	Ser	Ala
Ala	Ser	Gly
Gly	Ala	Val
Val	Phe	Arg
Arg	Ser	Ser
Ser	Lys	Lys
Lys	250	255
250	255	260
Val	Val	Val
Val	Ser	Leu
Leu	Pro	Thr
Thr	Thr	Leu
Leu	Tyr	Pro
Pro	Thr	Leu
Leu	Thr	Phe
Phe	Ser	
265	270	275
265	270	280
Pro	Pro	Leu
Leu	Pro	Ala
Ala	Glu	Lys
Lys	Gln	Ala
Ala	Leu	Ala
Ala	Glu	Asn
Asn	Ser	Ile
Ile	285	290
285	290	295
Gly	Tyr	Tyr
Tyr	Ser	Lys
Lys	Ile	Val
Val	Phe	Val
Val	Trp	Asp
Asp	Lys	Pro
Pro	Trp	Trp
Trp	Arg	
300	305	310
300	305	310
Glu	Gln	Gly
Gly	Phe	Ser
Ser	Gly	Val
Val	Leu	Gln
Gln	Ser	Ser
Ser	Cys	Asp
Asp	Pro	Ile
Ile	Ser	Ser
Ser	315	320
315	320	325
Phe	Ala	Arg
Arg	Asp	Thr
Thr	Ser	Ile
Ile	Asp	Asp
Asp	Val	Arg
Arg	Gln	Trp
Trp	Ser	Ser
Ser	Ile	Thr
330	335	340
330	335	340
Cys	Phe	Met
Met	Val	Gly
Gly	Asp	Pro
Pro	Gly	Arg
Arg	Lys	Trp
Trp	Ser	Gln
Gln	Gln	Ser
Ser	345	355
345	355	360
Gln	Val	Arg
Arg	Gln	Lys
Lys	Ser	Val
Val	Trp	Asp
Asp	Gln	Leu
Leu	Arg	Ala
Ala	Ala	Tyr
Tyr	Glu	
365	370	375
365	370	375
Asn	Ala	Gly
Gly	Ala	Gln
Gln	Val	Pro
Pro	Glu	Pro
Ala	Asn	Val
Val	Leu	Glu
Glu	380	385
380	385	390
Trp	Ser	Lys
Lys	Gln	Gln
Gln	Tyr	Phe
Phe	Gly	Ala
Ala	Pro	Ser
Ser	Ala	Val
Val	Tyr	Gly
395	400	405
395	400	405
Leu	Asn	Asp
Asp	Leu	Ile
Ile	Thr	Leu
Leu	Gly	Ser
Ser	Ala	Leu
Leu	Arg	Thr
Arg	Thr	Pro
Pro	Phe	Lys
410	415	420
410	415	420
Ser	Val	His
His	Phe	Val
Val	Gly	Thr
Thr	Glu	Thr
Thr	Ser	Leu
Leu	Val	Trp
Trp	Lys	Gly
Gly	Tyr	
425	430	435
425	430	440
Met	Glu	Gly
Gly	Ala	Ile
Ile	Arg	Ser
Ser	Gly	Gln
Gln	Arg	Gly
Gly	Ala	Ala
Ala	Glu	Val
Val	445	450
445	450	455
Ala	Ser	Ile
Ile	Val	Pro
Pro	Ala	Ala
Ala	460	

<210> 22
 <211> 1803
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> CDS
 <222> (1)...(1800)

<400> 22

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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val 20 25 30	96
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35 40 45	144
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50 55 60	192
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr 65 70 75 80	240
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly 85 90 95	288
ctg aag gct acc ttt gcc ctt gac agg ctc cct tgc acg ctg gtg Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val 100 105 110	336
cca gtg tgg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala 115 120 125	384
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val 130 135 140	432
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 145 150 155 160	480
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 165 170 175	528
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 180 185 190	576
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195 200 205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220	672
act gga aat tca atc cat caa gca caa gac ggt acat acc act acat gcf Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala	720

225	230	235	240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala				768
245	250	255		
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln				816
260	265	270		
gac ctc aag gcg aac cct cag gcg aag cgg ctc gac agt gtt agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe				864
275	280	285		
gct cac tac tgg gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val				912
290	295	300		
gca aac cag atc aca cgc gct ctg ctc ggt gtt gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Ala His Glu Ile				960
305	310	315	320	
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser				1008
325	330	335		
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys				1056
340	345	350		
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro				1104
355	360	365		
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala				1152
370	375	380		
tcc ggc tgg aca gta cga tcg gcc tcg ggc gcc gtt ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys				1200
385	390	395	400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe				1248
405	410	415		
tca cca cct ctt ccc gcc gag aag caa gca ttg ggc gaa aat tcc atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile				1296
420	425	430		
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp				1344
435	440	445		
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgg gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile				1392
450	455	460		

tca tcc gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	465	470	475	480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	485	490	495		1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	500	505	510		1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	515	520	525		1584
gag tgg tgg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	530	535	540		1632
ggg ctg aac gat ctc acc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	545	550	555	560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	565	570	575		1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	580	585	590		1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala	595	600			1803

<210> 23
 <211> 600
 <212> PRT
 <213> *Exophiala spinifera*

<400> 23
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 30

115	120	125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		
130	135	140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
145	150	155
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		160
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		
180	185	190
Asn Asp Leu Cys Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val		
195	200	205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr		
210	215	220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala		
225	230	235
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala		240
245	250	255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln		
260	265	270
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe		
275	280	285
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val		
290	295	300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Ala His Glu Ile		
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser		320
325	330	335
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys		
340	345	350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro		
355	360	365
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala		
370	375	380
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys		
385	390	395
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe		400
405	410	415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile		
420	425	430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp		
435	440	445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile		
450	455	460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile		
465	470	475
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser		480
485	490	495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr		
500	505	510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
515	520	525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
530	535	540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
545	550	555
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		560
565	570	575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		

580	585	590	
Val Ala Ser Leu Val Pro Ala Ala			
595	600		
<pre> <210> 24 <211> 3003 <212> DNA <213> Unknown </pre>			
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<pre> <221> sig_peptide <222> (1)...(72) <223> Barley alpha amylase signal sequence </pre>			
<pre> <221> misc_feature <222> (73)...(1575) <223> espl mat </pre>			
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<pre> <221> misc_feature <222> (1612)...(1614) <223> Extra lysine </pre>			
<pre> <400> 24 </pre>			
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<pre> ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96 Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala -5 1 5 </pre>			
<pre> ggc atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144 Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr 10 15 20 </pre>			
<pre> gtc agc gag ttc ttc ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe 25 30 35 40 </pre>			
<pre> gct cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr 45 50 55 </pre>			

gca tat ggt cca gca tgc ccc caa caa ttc aat tat ccc gaa gaa ctc Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu 60 65 70	288
sgt gag aat acg atg gca tgg ttc aat aca ccc ccc tca gct ggt Arg Glu Ile Thr Met Ala Try Phe Asn Thr Pro Pro Ser Ala Gly 75 80 85	336
gaa aat gag gac tgc ccc aac ccc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu 90 95 100	384
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gca gct gaa Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu 105 110 115 120	432
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct aat ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala 125 130 135	480
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu 140 145 150	528
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly 155 160 165	576
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala 170 175 180	624
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala 185 190 195 200	672
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro 205 210 215	720
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe 220 225 230	768
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtc caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Val Gln Ala Leu 235 240 245	816
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp 250 255 260	864
ctc gcc act ctc atg aac acg atc gag cca ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Phe Glu 265 270 275 280	912
taa acg ttg gac aac gta acg gct gtc tac cgt tct gaa acg gct cgc	960

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg			
285	290	295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc			1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala			
300	305	310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat			1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Asn Asp Thr Gln Ala Tyr			
315	320	325	
ctc gag gag gca atc ccc aat cag ccc gac ctt tac cag act ctc ctt			1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu			
330	335	340	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag			1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln			
345	350	355	360
att gcc gcc att gag acc gag gta aga ttc cag tgc cct tct gcc atc			1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
365	370	375	
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac			1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
380	385	390	
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg			1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
395	400	405	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca			1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
410	415	420	
agt gcg acc gcc ttg gag gcc cag acg acg aaa tac atg cag ggt gcc			1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
425	430	435	440
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa			1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
445	450	455	
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt			1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
460	465	470	
gac gtc tct cca gcg aca ata gac caa cga tgc gcc ttg tac acg cgt			1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
475	480	485	
tat tat act gag ttg ggc aca atc gcg ccc agg aca ttt ggc gga ggc			1584
Tyr Tyr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
490	495	500	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg			1632
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
505	510	515	520

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535	1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag ggc atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550	1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555 560 565	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Gln Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca	2352

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
745	750	755	760
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aac			2400
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
765	770	775	
aag gtg gtc gtt tcg tca ccg aca acc ttg tat ccc acc ttg aca ttt			2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
780	785	790	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
795	800	805	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccc tgg tgg			2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
810	815	820	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			2592
Arg Glu Gin Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
825	830	835	840
tca ttg gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
845	850	855	
acc tgt ttc atg gtc gga gac ccg gga ccg aag tgg tcc caa cag tcc			2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
860	865	870	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac			2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
875	880	885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc			2784
Glu Asn Ala Gly Ala Gln Val Pro Gln Pro Ala Asn Val Leu Glu Ile			
890	895	900	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat			2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
905	910	915	920
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc			2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
925	930	935	
aag agt gtt cat ttc gtt gga acg gag acg tct tca gtt tgg aaa ggg			2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
940	945	950	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt			2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
955	960	965	
gtg gct agc ctg gtc cca gca gca tag			3003
Val Ala Ser Leu Val Pro Ala Ala			

970

975

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 <211> 1000
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(24)

<400> 25

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 Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
 -5 1 5
 Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
 25 30 35 40
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
 45 50 55
 Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
 60 65 70
 Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
 75 80 85
 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
 90 95 100
 Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
 105 110 115 120
 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
 125 130 135
 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
 140 145 150
 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
 155 160 165
 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
 170 175 180
 Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
 185 190 195 200
 Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
 205 210 215
 Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
 220 225 230
 Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
 235 240 245
 Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
 250 255 260
 Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
 265 270 275 280
 Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
 285 290 295
 Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
 300 305 310
 Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
 315 320 325
 Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu

330	335	340
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln		
345	350	355
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile		360
365	370	375
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr		
380	385	390
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val		
395	400	405
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala		
410	415	420
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala		
425	430	435
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln		440
445	450	455
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val		
460	465	470
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg		
475	480	485
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly		
490	495	500
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val		
505	510	515
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		520
525	530	535
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
540	545	550
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		
555	560	565
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val		
570	575	580
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr		
585	590	595
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala		
605	610	615
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala		
620	625	630
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln		
635	640	645
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe		
650	655	660
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val		
665	670	675
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile		680
685	690	695
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser		
700	705	710
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys		
715	720	725
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro		
730	735	740
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala		
745	750	755
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys		760
765	770	775
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe		
780	785	790
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile		

795	800	805
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp		
810	815	820
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile		
825	830	835
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile		
845	850	855
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser		
860	865	870
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr		
875	880	885
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
890	895	900
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
905	910	915
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
925	930	935
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
940	945	950
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		
955	960	965
Val Ala Ser Leu Val Pro Ala Ala		
970	975	

<210> 26

<211> 2976

<212> DNA

<213> Unknown

<220>

<223> Barley alpha amylase signal sequence: BEST1
mature: artificial spacer: and K:trAPAO. For
plant expression.

<221> sig_peptide

<222> (1)...(72)

<223> Barley alpha amylase signal sequence

<221> mat_peptide

<222> (73)...(1545)

<223> BEST1 mature

<221> misc_feature

<222> (1546)...(1584)

<223> spacer sequence

<221> misc_feature

<222> (1585)...(2973)

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<221> CDS

<222> (1)...(2973)

<221> misc_feature

<222> (1585)...(1587)

<223> Extra lysine

<400> 26

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly 48
-20 -15 -10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt cct gtc cgc agg acc
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr 96
-5 1 5

gat ctg ggc cag gtc cag gga ctg gcc ggg gac gtg atg aac ttt cgc
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg 144
10 15 20

gga ata ccc tat gca gcg ccc gtc ggg ctg cgt tgg aag ccc
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro 192
25 30 35 40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe 240
45 50 55

ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc aac ctc gcc
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala 288
60 65 70

ccc ggc gtg aac gac tgc ttt tac ctc aac gta tgg gcg cog tca
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser 336
75 80 85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly 384
90 95 100

ggc ttc gcc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg
Gly Phe Ala Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala 432
105 110 115 120

ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn 480
125 130 135

atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag aac ccc acc
Ile Leu Gly Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr 528
140 145 150

gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg 576
155 160 165

tgg ggg cag aac ggc cgc gcc ttc gga ggg gac ccc ggc cga gtg
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val 624
170 175 180

acg gtc ttt ggt gaa tcg gcc gga gcg aac ggg atc gga ctt ctg ctc
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu 672
185 190 195 200

acc tcc ccg ctg aac aag ggt ctc ttc cgt ggc gct atc ctc gaa aac	720		
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser			
205	210	215	
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac aac gcc gcc tcc	768		
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser			
220	225	230	
ggc gag cgc ctc gac gcc gat ctt tcc cga ctg cgc tcc acc gac cca	816		
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro			
235	240	245	
gcc acc ctg atg gcc cgc gcc gac gcc gcc ccc gca tcc cgg gac	864		
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp			
250	255	260	
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat gcc cat gtg ctc	912		
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu			
265	270	275	280
ccg cag acc gac aac gcc gcc gac gcc gcc ggg cag ctg gcc ccc gtt	960		
Pro Gln Thr Asp Ser Ala Ala Ile Ala Gly Gln Leu Ala Pro Val			
285	290	295	
ccg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg	1008		
Arg Val Leu Ile Gly Thr Asp Ala Asp Glu Gly Arg Ala Phe Leu Gly			
300	305	310	
cgc gcc ccg atg gag acg cca gcc gac tac caa gcc tat ctg gag gcc	1056		
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala			
315	320	325	
cag ttt ggc gac caa gcc gcc gtc gtg gcc gtc tat ccc ccc gac	1104		
Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp			
330	335	340	
ggc cgg gcc acg ccc aag gaa atg gtc gcc gtc atc ttc ggc gac aat	1152		
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn			
345	350	355	360
cag ttc aat cgg egg gtc tcc gcc tcc tcc gaa gcc ctt gtg ccc cag	1200		
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln			
365	370	375	
ggc gcc ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248		
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly			
380	385	390	
aga gcc ccg gct acc cac gga gcc gaa att ccc tac gtt tcc ggg gtg	1296		
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val			
395	400	405	
tcc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344		
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro			
410	415	420	
acg ccc gcc gac cgt gcc ctg ggc caa ctg atg tcc tcc gcc cgg gtc	1392		
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val			

425	430	435	440	
cgg ttc gcc aag aat ggc gac ccc gac ggg gac gcc ctt acc tgg cct Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro				1440
445		450	455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg				1488
460		465	470	
gcg gcg gtg gtc ccc gga cct tcc atc ccc cct tgc gcg gat ggc Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly				1536
475		480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser				1584
490		495	500	
aaa gac aac gtt gcg gac gtg gta gtg ggc gct ggc ttg agc ggt Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly				1632
505		510	515	520
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtc Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val				1680
525		530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				1728
540		545	550	
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				1776
555		560	565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				1824
570		575	580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				1872
585		590	595	600
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				1920
605		610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				1968
620		625	630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				2016
635		640	645	
cgg ctc gac agt ttg agc ttc gcg ccc tac tgc gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				2064
650		655	660	

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gin Ile Thr Arg Ala Leu Leu 665 670 675 680	2112
ggt gtg gaa gcc cac gag atc aac atg ctt ttc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 685 690 695	2160
aag aat gcc acc ggt ctc aat aat ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700 705 710	2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 715 720 725	2256
aat tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 730 735 740	2304
gct gaa att gag cag tcg gca tcc ggc ttt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 745 750 755 760	2352
ggc gcc gtg ttc cga aac aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr 765 770 775	2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780 785 790	2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 795 800 805	2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 810 815 820	2544
caa tcg aac ttt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825 830 835 840	2592
gtc gat cga caa tgg tcc att acc ttt atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845 850 855	2640
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 860 865 870	2688
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 875 880 885	2736
ccg gcc aac gtg ttc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	2784

890	895	900																																																																																																																	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			2832																																																																																																																
905	910	915	920																																																																																																																
tcg ccg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			2880																																																																																																																
925	930	935																																																																																																																	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			2928																																																																																																																
940	945	950																																																																																																																	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			2973																																																																																																																
955	960	965																																																																																																																	
tag			2976																																																																																																																
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<ul style="list-style-type: none"> <400> 27 																																																																																																																			
<table border="0"> <tbody> <tr> <td>Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">-20</td> <td style="text-align: center;">-15</td> <td style="text-align: center;">-10</td> <td></td> </tr> <tr> <td>Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">-5</td> <td style="text-align: center;">1</td> <td style="text-align: center;">5</td> <td></td> </tr> <tr> <td>Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">10</td> <td style="text-align: center;">15</td> <td style="text-align: center;">20</td> <td></td> </tr> <tr> <td>Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">25</td> <td style="text-align: center;">30</td> <td style="text-align: center;">35</td> <td style="text-align: center;">40</td> </tr> <tr> <td>Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">45</td> <td style="text-align: center;">50</td> <td style="text-align: center;">55</td> <td></td> </tr> <tr> <td>Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">60</td> <td style="text-align: center;">65</td> <td style="text-align: center;">70</td> <td></td> </tr> <tr> <td>Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">75</td> <td style="text-align: center;">80</td> <td style="text-align: center;">85</td> <td></td> </tr> <tr> <td>Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">90</td> <td style="text-align: center;">95</td> <td style="text-align: center;">100</td> <td></td> </tr> <tr> <td>Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">105</td> <td style="text-align: center;">110</td> <td style="text-align: center;">115</td> <td style="text-align: center;">120</td> </tr> <tr> <td>Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">125</td> <td style="text-align: center;">130</td> <td style="text-align: center;">135</td> <td></td> </tr> <tr> <td>Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">140</td> <td style="text-align: center;">145</td> <td style="text-align: center;">150</td> <td></td> </tr> <tr> <td>Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">155</td> <td style="text-align: center;">160</td> <td style="text-align: center;">165</td> <td></td> </tr> <tr> <td>Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">170</td> <td style="text-align: center;">175</td> <td style="text-align: center;">180</td> <td></td> </tr> <tr> <td>Tyr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu</td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: center;">185</td> <td style="text-align: center;">190</td> <td style="text-align: center;">195</td> <td style="text-align: right;">200</td> </tr> </tbody> </table>				Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly				-20	-15	-10		Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr				-5	1	5		Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg				10	15	20		Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro				25	30	35	40	Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe				45	50	55		Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala				60	65	70		Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser				75	80	85		Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly				90	95	100		Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala				105	110	115	120	Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn				125	130	135		Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr				140	145	150		Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg				155	160	165		Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val				170	175	180		Tyr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu				185	190	195	200
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155	160	165																																																																																																																	
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val																																																																																																																			
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Tyr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu																																																																																																																			
185	190	195	200																																																																																																																

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
 205 210 215
 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
 220 225 230
 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
 235 240 245
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
 250 255 260
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 Pro Gln Thr Asp Ser Ala Ala Ile Ala Gly Gln Leu Ala Pro Val
 285 290 295
 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
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 Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
 330 335 340
 Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
 345 350 355 360
 Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
 365 370 375
 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
 380 385 390
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
 395 400 405
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
 410 415 420
 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
 425 430 435 440
 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
 445 450 455
 Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
 460 465 470
 Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
 475 480 485
 Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser
 490 495 500
 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
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 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 525 530 535
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 540 545 550
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
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 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
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 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 605 610 615
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 620 625 630
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 635 640 645
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 650 655 660

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 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 685 690 695
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 700 705 710
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 715 720 725
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 730 735 740
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 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 780 785 790
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 795 800 805
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
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 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 825 830 835 840
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 845 850 855
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 860 865 870
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 875 880 885
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 890 895 900
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
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 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
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 955 960 965

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 <212> DNA
 <213> Unknown

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 2227-3615, K:trAPAO, 3616-3618, stop codon. For
 bacterial expression.

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act	cga	ctt	ctt	ttg	gaa	tat	ctt	gaa	aaa	tat	gaa	gag	cat	ttg	96
Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
20				25						30					

tat	gag	ccg	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Phe	Glu	Leu		
35				40					45							

ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	ttt	aaa	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
50			55						60							

tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tac	ata	gct	gac	aag	cac	aac	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65				70					75			80				

atg	ttg	ggt	ttt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288
Met	Leu	Gly	Gly	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
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gga	gct	gtt	ttg	gat	att	aga	tac	ggt	ttc	aga	att	gca	tat	agt	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
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aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
115			120						125							

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Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
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															47	

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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttc cag ggc tgg caa gcc			624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
acg ttt ggt ggc gac cat cct cca aza tcg gat ctg gtt ccc cgt			672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
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Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val			
225	230	235	240
gtc ggc acg act act gtc ccc ggc acc act gcc acc gtc agc gag			768
Val Gly Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu			
245	250	255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccc aca cga ttt gcg cct cct			816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro			
260	265	270	
act cgt ccc gtc cct tgg tca acg cct ttg caa gcc act gca tat ggt			864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly			
275	280	285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att			912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile			
290	295	300	
acg atg gcc tgg ttc aat aca ccc ccc tca gct ggt gaa agt gag			960
Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly Glu Ser Glu			
305	310	315	320
gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac			1008
Asp Cys Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn			
325	330	335	
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Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp			
355	360	365	
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Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro			
370	375	380	
gct gcc cct cag ctt cca aat aca cag cga aat ctg ggg ttc cta gac			1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp			
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ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420	425	430	1296	
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acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485	490	495	1488	
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Phe Glu Tyr Thr Leu 500	505	510	1536	
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act gct Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly 515	520	525	1584	
gac att gct cgt gta cct gtc ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530	535	540	1632	
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545	550	555	560	1680
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ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580	585	590	1776	
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595	600	605	1824	
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610	615	620	1872	
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac aac 49			1920	

Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser			
625	630	635	640
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gct acc			1968
Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr			
645	650	655	
gcc ttg gag gcc cag acg acc aaa tac atg cag ggt gcc tgg gct gcc			2016
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala			
660	665	670	
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtc ccg aat			2064
Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn			
675	680	685	
gtc gct gct ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct			2112
Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser			
690	695	700	
cca gct aca ata gac caa cga ttt gtc ttt tac acg cgt tat tat act			2160
Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr			
705	710	715	720
gag ttg ggc aca atc gct ccg agg aca ttt ggc gga ggc agc ggc gga			2208
Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly			
725	730	735	
ggc aca ggc gga ggc agc aaa gac aac gtt gct gac gtg gta gtg gtg			2256
Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val			
740	745	750	
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc			2304
Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala			
755	760	765	
ggt ctg tcc tgc ctc gtt ctt gag gct atg gat cgt gta ggg gga aag			2352
Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys			
770	775	780	
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Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu			
785	790	795	800
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805	810	815	
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tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt			2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly			
835	840	845	
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gct gaa ctc ctc			2592
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu			
850	855	860	

ccc gta tgg tct cag ctc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
tgt gag aag gaa cta zac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 910	2736
atc aca cgc gct ctc ggt gtg gaa gcc cac gag atc agc atg ctc Ile Thr Arg Ala Leu Leu Gly Val Ala His Glu Ile Ser Met Leu 915 920 925	2784
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe 930 935 940	2832
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met 945 950 955 960	2880
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg Gin Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val 965 970 975	2928
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys 980 985 990	2976
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val 995 1000 1005	3024
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro 1010 1015 1020	3072
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr 1025 1030 1035 1040	3120
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln 1045 1050 1055	3168
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala 1060 1065 1070	3216
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe 1075 1080 1085	3264
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta	3312

Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
 1090 1095 1100

cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc 3360
 Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
 1105 1110 1115 1120

ggg gcc cza gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg 3408
 Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
 1125 1130 1135

aaç cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac 3456
 Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
 1140 1145 1150

gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt 3504
 Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
 1155 1160 1165

cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa 3552
 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
 1170 1175 1180

ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc 3600
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 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
 225 230 235 240
 Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
 245 250 255
 Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
 260 265 270
 Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
 275 280 285
 Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
 290 295 300
 Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly Glu Ser Glu
 305 310 315 320
 Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
 325 330 335
 Lys Ala Val Met Val Trp Ile Tyr Gly Ala Leu Glu Tyr Gly Trp
 340 345 350
 Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
 355 360 365
 Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro
 370 375 380
 Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp
 385 390 395 400
 Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly
 405 410 415
 Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg
 420 425 430
 Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg
 435 440 445
 Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly
 450 455 460
 Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr
 465 470 475 480
 Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Asn Thr
 485 490 495
 Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu
 500 505 510
 Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly
 515 520 525
 Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly
 530 535 540
 Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu
 545 550 555 560
 Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr
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 Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala
 580 585 590
 Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln
 595 600 605
 Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala
 610 615 620

Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser
 625 630 635 640
 Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr
 645 650 655
 Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala
 660 665 670
 Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn
 675 680 685
 Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser
 690 695 700
 Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr
 705 710 715 720
 Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly
 725 730 735
 Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val
 740 745 750
 Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala
 755 760 765
 Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys
 770 775 780
 Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu
 785 790 795 800
 Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu
 805 810 815
 Phe Glu Arg Phe His Leu Glu Gly Gln Leu Gln Arg Thr Thr Gly Asn
 820 825 830
 Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly
 835 840 845
 Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
 850 855 860
 Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys
 865 870 875 880
 Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr
 885 890 895
 Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln
 900 905 910
 Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu
 915 920 925
 Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe
 930 935 940
 Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met
 945 950 955 960
 Gln Ser Ile Cys His Ala Met Ser Lys Gln Leu Val Pro Gly Ser Val
 965 970 975
 His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
 980 985 990
 Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val
 995 1000 1005
 Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro
 1010 1015 1020
 Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr
 1025 1030 1035 1040
 Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln
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 Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala
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 Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Trp Cys Phe
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Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
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 Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
 1105 1110 1115 1120
 Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
 1125 1130 1135
 Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
 1140 1145 1150
 Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
 1155 1160 1165
 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
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 Leu Val Pro Ala Ala
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 bacterial expression vector pGEX-4T-1 or similar
 vector. gst:BEST1:sp:K:trAPAO fusion, 3591 nt.
 1-687 gst
 + polylinker, 688-2163, BEST1 mature, 2164-2199,
 spacer, 2200-3588, K:trAPAO

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1

5

10

15

55

49

act cga ctt ctc tct gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gat aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg ccc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgg cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtc ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttg ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgg cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat ggc ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgg ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	575
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctt gtt ccg cgt	672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc acg gat ttt ccg gtc ccg agg acc gat ctg ggc	720
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	
225 230 235 240	
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt ccg gga ata ccc	768
56	

Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro			
245	250	255	
tat gca gcg ccg ccc gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac			816
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His			
260	265	270	
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac			864
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp			
275	280	285	
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg			912
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val			
290	295	300	
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa			960
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys			
305	310	315	320
ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc			1008
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala			
325	330	335	
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag ggc ctt gcg cga			1056
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Gln Ala Leu Ala Arg			
340	345	350	
cag ggc gtc gtc gtg gtc acg ttt aac tat cgg acg aac atc ctg ggc			1104
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly			
355	360	365	
tct ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg			1152
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser			
370	375	380	
ggc aac tac ggc cta ctc gac atc ctc gcc gct ctt cgg tgg gtg cag			1200
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln			
385	390	395	400
acg aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt			1248
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe			
405	410	415	
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg			1296
Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro			
420	425	430	
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg			1344
Leu Ser Lys G'y Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu			
435	440	445	
acg cga ccg ctc gcg acg ctc gcc gac agc gcc ggc tgg ggc gag cgc			1392
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg			
450	455	460	
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg			1440
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu			
465	470	475	480

atg	gct	cgc	gcc	gac	gct	gct	ccg	gac	ctg	cgc	agg	1488					
Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	Leu	Arg	Arg		
485									490				495				
ccg	cgt	ccg	acc	gga	ccg	atc	gtc	gat	ggc	cat	gtg	ctg	ccg	cag	acc	1536	
Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr		
500						505					510						
gac	agc	gct	gct	atc	gct	gct	ggg	cag	ctg	gct	ccg	ccg	gtt	ccg	gtc	ctg	1584
Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu		
515							520				525						
atc	gga	acc	aat	gcc	gac	gaa	ggc	cgc	gcc	tcc	ctc	ggg	cgc	gct	ccg	1632	
Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro		
530					535					540							
atg	gag	acg	cca	gct	gac	tac	caa	gcc	tat	ctg	gag	gct	cag	ttt	ggc	1680	
Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly		
545					550				555		560						
gac	caa	gcc	gcc	gtg	gct	gct	tat	ccc	ctc	gac	ggc	ccg	gac	ggc	ggc	1728	
Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala		
565						570					575						
acg	ccc	aa	gaa	atg	gtc	gct	ccg	cgc	atc	tcc	ggc	gac	aat	cag	tcc	1776	
Thr	Pro	Lys	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn			
580					585					590							
cg	ggg	gtc	tcc	tcc	tcc	gaa	gct	ctt	gtg	cgc	cag	ggc	ccg	ccg	1824		
Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro		
595					600				605								
gtg	tgg	cgt	tat	cag	tcc	aac	gg	aat	acc	gag	gg	gga	aga	gct	ccg	1872	
Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro		
610					615				620								
gct	acc	cac	gga	gaa	att	ccc	tac	gtt	tcc	ggg	gtg	tcc	aag	c	1920		
Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu		
625					630				635		640						
gac	gag	ttg	gg	ctg	tcc	gat	tgg	ccg	ccc	gag	ggg	ccc	acg	ccc	gcc	1968	
Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala		
645					650				655								
gac	cgt	ccg	ccg	caa	ctg	atg	tcc	tcc	gcc	tgg	gtc	ccg	tcc	gcc	2016		
Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala		
660					665				670								
aag	aat	ggc	gac	ccc	ggc	gg	gac	ggc	ctt	acc	tgg	cct	gcc	tat	tct	2064	
Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser		
675					680				685								
acg	ggc	aag	tcc	acc	atg	aca	tcc	gg	ccc	gag	ggc	ccg	ccg	ccg	gtg	2112	
Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	Ala	Ala	Val		
690					695				700								
gtg	tcc	ccc	gga	cct	tcc	atc	ccc	cc	tcc	gct	gag	ggc	gcc	aag	ggc	2160	

Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala	705	710	715	720
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac				3208
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn				
725	730	735		
gtt gcg gac gtg gta gtc gtc gtc gct ggc ttg agc ggt ttg gag aca				3256
Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr				
740	745	750		
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg				3304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala				
755	760	765		
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc				3352
Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly				
770	775	780		
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac				3400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn				
785	790	795	800	
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag				3448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu				
805	810	815		
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca				3496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr				
820	825	830		
acc act aca gct tat ggt gac tcc ttg ctg agc gag gag gtt gca				3544
Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala				
835	840	845		
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag				3592
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu				
850	855	860		
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac				3640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp				
865	870	875	880	
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct				3688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala				
885	890	895		
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa				3736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu				
900	905	910		
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc				3784
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala				
915	920	925		
acc ggt ctc agt aat att ttc tcc gac aag aaa gac ggc ggg cag tat				3832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr				
930	935	940		

atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg cca aag Met Arg Cys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys 945 950 955 960	7880
gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile 965 970 975	7928
gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc stg Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val 980 985 990	7976
ttc cga agc aaa aag gtc gtg gtt tcg tta ccg aca acc ttg tat ccc Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro 995 1000 1005	8024
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala 1010 1015 1020	8072
gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp 1025 1030 1035 1040	8120
aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser 1045 1050 1055	8168
tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg 1060 1065 1070	8216
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp 1075 1080 1085	8264
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu 1090 1095 1100	8312
cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn 1105 1110 1115 1120	8360
gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro 1125 1130 1135	8408
agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcc ctc Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu 1140 1145 1150	8456
aga acg ccg ttc aag agt gtt cat ttc gga acg gag acg tct tta Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu 1155 1160 1165	8504
gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt 60	3552

Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
 1170 1175 1180

gct gca gaa gtt gtg gct agc ctg ctg cca gca gca tag 3591
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 1185 1190 1195

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 <211> 1196
 <212> PRT
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 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Glu Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
 225 230 235 240
 Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
 245 250 255
 Tyr Ala Ala Pro Pro Val Gly Leu Arg Trp Lys Pro Pro Gln His
 260 265 270
 Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
 275 280 285
 Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
 290 295 300
 Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
 305 310 315 320
 Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala
 325 330 335
 GLY GLY TYR Ala Ala Met Pro Tyr Tyr Asp GLY Glu Ala Leu Ala Arg
 340 345 350

Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
 355 360 365
 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
 370 375 380
 Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
 385 390 395 400
 Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
 405 410 415
 Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
 420 425 430
 Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
 435 440 445
 Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
 450 455 460
 Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu
 465 470 475 480
 Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg
 485 490 495
 Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr
 500 505 510
 Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu
 515 520 525
 Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro
 530 535 540
 Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly
 545 550 555 560
 Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala
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 Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn
 580 585 590
 Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro
 595 600 605
 Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro
 610 615 620
 Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu
 625 630 635 640
 Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala
 645 650 655
 Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala
 660 665 670
 Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser
 675 680 685
 Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val
 690 695 700
 Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala
 705 710 715 720
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Lys Asp Asn
 725 730 735
 Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr
 740 745 750
 Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala
 755 760 765
 Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly
 770 775 780
 Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn
 785 790 795 800
 Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Gln Gly Glu
 805 810 815

Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr
 820 825 830
 Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala
 835 840 845
 Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu
 850 855 860
 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
 865 870 875 880
 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
 885 890 895
 Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu
 900 905 910
 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
 915 920 925
 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
 930 935 940
 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
 945 950 955 960
 Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
 965 970 975
 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
 980 985 990
 Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
 995 1000 1005
 Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala
 1010 1015 1020
 Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp
 1025 1030 1035 1040
 Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser
 1045 1050 1055
 Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg
 1060 1065 1070
 Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
 1075 1080 1085
 Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu
 1090 1095 1100
 Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
 1105 1110 1115 1120
 Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
 1125 1130 1135
 Ser Ala Val Tyr Leu Asn Asp Leu Ile Thr Leu Cys Ser Ala Leu
 1140 1145 1150
 Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
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 1185 1190 1195

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 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1803)

<223> Glyc(-)APAO coding sequence; mutation in putative glycosylation sites

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gca ggg tat tct ccc gtc ggc gta ggc cca gac gga ggg agg tat gtg 96
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30

aca ata gct gga cag att gga caa gac gct tcc ggc gtg aca gac cct 144
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc 192
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac 240
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg 288
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95

ctg aag gct acc ttt gcc ctt gac agg ctc cct tgc acg ctg gtg 336
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc 384
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg 432
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
 130 135 140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc 480
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160

cag gcc gcc ggt ctg tcc ctc gtt ctt gag gca atg gat cgt gta 528
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175

ggg gga aag act ctg agc gta caa tcc ggt ccc ggc agg acg act acc 576
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190

aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta 624
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
 195 200 205

tcc aga ttg tct gaa aga ttt cat ttg gag ggc gag ccc cag agg acg 672
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr

210	215	220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct			720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala			
225	230	235	240
ctt tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg			768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
245	250	255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa			816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
260	265	270	
gac ctc aag gcg aac cct cag gcg aag cgg ctc gac agt gtg agc ttc			864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
275	280	285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta			912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
290	295	300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc			960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
305	310	315	320
agc atg ctt ttt ctc acc gac tac atc aag agt gac acc ggt ctc agt			1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
325	330	335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa			1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
340	345	350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca			1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
355	360	365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca			1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
370	375	380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa			1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
385	390	395	400
aag gtg gtg gtt tcg tta ccc aca acc ttg tat ccc acc ttg aca ttc			1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
405	410	415	
tca cca cct ctt ccc gcc gag aag caa gca ttg ggc gaa aat tct atc			1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
420	425	430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccc tgg tgg			1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
435	440	445	

ccg gaa caa ggc ttc tcc ggc gtc ctc caa tcg agc tgc gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
gag aac gcc cgg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530 535 540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
tat atg gaa ggg gcc ata cga tcg ggc caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gln Arg Gly Ala Ala Glu Val 580 585 590	1776
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595 600	

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<212> PRT
<213> Unknown

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Thr Ile Ala Gly Gln Ile Gly Cln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
66

85	90	95
Leu Lys Ala Thr Phe Ala Leu Asp Arg	Leu Pro Pro Cys Thr	Leu Val
100	105	110
Pro Val Ser Ala Leu Ser Ser	Pro Glu Tyr Leu Phe	Glu Val Asp Ala
115	120	125
Thr Ala Leu Val Pro Gly	His Thr Thr Pro Asp Asn	Val Ala Asp Val
130	135	140
Val Val Val Gly Ala Gly	Leu Ser Gly	Leu Thr Ala Arg Lys Val
145	150	155
Gln Ala Ala Gly	Leu Ser Cys	Leu Val Leu Glu Ala Met Asp Arg Val
165	170	175
Gly Gly Lys Thr Leu Ser Val	Gln Ser Gly	Pro Gly Arg Thr Thr Ile
180	185	190
Asn Asp Leu Gly Ala Ala	Trp Ile Asn Asp Ser Asn	Gln Ala Glu Val
195	200	205
Ser Arg Leu Phe Glu Arg	Phe His Leu Glu Gly	Glu Leu Gln Arg Thr
210	215	220
Thr Gly Asn Ser Ile	His Gln Ala Gln Asp	Gly Thr Thr Thr Ala
225	230	235
Pro Tyr Gly Asp Ser	Leu Leu Ser Glu	Glu Val Ala Ser Ala Leu Ala
245	250	255
Glu Leu Leu Pro Val Trp Ser	Gln Leu Ile Glu Glu His	Ser Leu Gln
260	265	270
Asp Leu Lys Ala Ser Pro	Gln Ala Lys Arg	Leu Asp Ser Val Ser Phe
275	280	285
Ala His Tyr Cys Glu Lys	Glu Leu Asn	Leu Pro Ala Val Leu Gly Val
290	295	300
Ala Asn Gln Ile Thr Arg	Ala Leu Leu Gly	Val Glu Ala His Glu Ile
305	310	315
Ser Met Leu Phe Leu Thr Asp	Tyr Ile Lys Ser	Ala Thr Gly Leu Ser
325	330	335
Asn Ile Phe Ser Asp Lys	Lys Asp Gly	Gly Gln Tyr Met Arg Cys Lys
340	345	350
Thr Gly Met Gln Ser Ile	Cys His Ala Met Ser Lys	Glu Leu Val Pro
355	360	365
Gly Ser Val His Leu Asn	Thr Pro Val Ala Glu Ile	Glu Gln Ser Ala
370	375	380
Ser Gly Cys Thr Val Arg	Ser Ala Ser Gly	Ala Val Phe Arg Ser Lys
385	390	395
Lys Val Val Val Ser	Leu Pro Thr Thr	Leu Tyr Pro Thr Leu Thr Phe
405	410	415
Ser Pro Pro Leu Pro Ala	Glu Lys Gln Ala	Leu Ala Glu Asn Ser Ile
420	425	430
Leu Gly Tyr Tyr Ser Lys	Ile Val Phe Val Trp Asp	Lys Pro Trp Trp
435	440	445
Arg Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser	Ser Cys Asp Pro Ile
450	455	460
Ser Phe Ala Arg Asp	Thr Ser Ile Asp Val	Asp Arg Gln Trp Ser Ile
465	470	475
Thr Cys Phe Met Val	Gly Asp Pro Gly	Arg Lys Trp Ser Gln Gln Ser
485	490	495
Lys Gln Val Arg Gln	Lys Ser Val Trp Asp	Gln Leu Arg Ala Ala Tyr
500	505	510
Glu Asn Ala Gly Ala Gln	Val Pro Gln Pro Ala Asn	Val Leu Glu Ile
515	520	525
Glu Trp Ser Lys Gln Gln	Tyr Phe Gln Gly	Ala Pro Ser Ala Val Tyr
530	535	540
Gly Leu Asn Asp Leu Ile	Thr Leu Gly Ser Ala	Leu Arg Thr Pro Phe

545 550 555 560
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
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 580 585 590
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 595 600

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<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 37-mer oligonucleotide

<400> 34

gggaaatcca tggcacttgc accgagctac atccaatc

37

<210> 35

<211> 1929

<212> DNA

<213> Exophiala spinifera

<220>

<221> intron

<222> (739)...(811)

<221> intron

<222> (1134)...(1186)

<400> 35

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gacgcgttgg	gcgttgacaga	cccagccctac	gagaaacagg	ttggcccaagc	atcgcccaat	180
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gaataacctct	ttggaggttga	tgcccaeggcg	ctgggtccag	gacactcgac	cccaagacaac	420
gttgcggacg	ttgttagtgt	gggcgttggc	ttgagcggtt	tggagacggc	acgcaaaagtc	480
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ctgagcgtac	atcggttccc	ggcaggacg	actatcaac	acctcggtgc	tgcgtggatc	600
aatgacagca	acccaaagcga	agtatccaga	ttgtttgaaa	gattttcattt	ggaggggcggag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtaacaac	cactacagct	720
ccttatggtg	actccccgtt	aagcacaatc	ccacttttgtt	atcgagaccc	tgcgtggatc	780
agaatacagt	cactgactcc	acttcgttcca	gtcgaggcgg	gagggttcaa	gtgcacttgc	840
ggaaccccttc	cccgatgtt	ctcagctgtat	cgaaatgtat	ayccattyaa	acccaaaggc	900
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taatattgtc	tcggacaaga	aagacggcgg	cgagtataat	cgatgcataaa	cagggtggcg	1140
cggtgttctc	tcaggtaggg	gactgtttc	ttaggtgtca	ttccaggat	gcagtcgatt	1200
tgcctatgcca	tgtcaaagg	actttttcca	ggctcagtgc	acctcaacac	cccggtcgct	1260
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ccttttcccg	ccgagaagca	agcattggcg	gaaaaatcta	tccctggctt	ctatagcaag	1440
atagtcttcg	taatggacaa	cccggtgtgg	cgcgaaacgg	gtttttcggy	ttttttccaa	1500
tcgagctgt	acccatctc	atttgccaga	gtatccagca	tgcgaaatcg	tcggcaatgg	1560

tccatcacct	gtttcatgtt	cgagaccccg	ggacggaaagt	ggtcccaaca	gtccaaaggcag	1620
gtacgacaaa	agtctgtctc	ggaccaactc	cgcgcagcct	acgagaacgc	cggggcccaa	1680
gtcccaagac	cgccaaactc	gatcgaaatc	gatgggtcga	agcagcagta	tttccaaggaa	1740
gtcccgagcg	ccgtctatgg	gatggaaacgt	catacacac	ttgggttcgc	gtccagaacg	1800
ccgttcaagt	gtgttcatti	cgatggaaacg	gagacgtctt	tagtttggaa	aggatataatg	1860
gaaggggcca	taatgtcggg	tcaacggat	gatgcagaag	ttgtggctag	cctgggtccca	1920
gcacatag						1929

<210> 36
 <211> 600
 <212> PRT
 <213> Exophiala spinifera

<400> 36						
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro						
1	5	10	15			
Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val						
20	25	30				
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro						
35	40	45				
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys						
50	55	60				
Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr						
65	70	75	80			
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly						
85	90	95				
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val						
100	105	110				
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala						
115	120	125				
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val						
130	135	140				
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val						
145	150	155	160			
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val						
165	170	175				
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile						
180	185	190				
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val						
195	200	205				
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr						
210	215	220				
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala						
225	230	235	240			
Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala						
245	250	255				
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu						
260	265	270				
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe						
275	280	285				
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val						
290	295	300				
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile						
305	310	315	320			
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser						
325	330	335				
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys						
340	345	350				

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 37
 <211> 1929
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1186)

<400> 37

atggcaacttg	cacccgagcta	catcaatccc	ccaaacgtcg	cctccccaggc	agggttattcc	60
cacatcgccg	taeggccaaa	cgaagcgagg	tatgtgacaa	tagctggaca	gatgtggacaa	120
gacgctttgg	gcgtgacaga	cccagccatc	gagaaaacagg	ttgccccaa	atccggccat	180
ctggcgagcc	gccttgcgtc	agttggagcc	tcttcacccg	ccgtccaccc	gtccaaattac	240
tacatcgctcg	actacgcccc	gagcaaaactc	accgcaatttg	gagatgggtt	gaagtcttacc	300
tttgccttgc	acaggctccc	tccttgcacg	ctgggtgcacg	tacccggcctt	ggcttcaccc	360
gaataccctc	ttgaggttga	cgcccaaggcg	ctgggtgcacg	gacacccgcac	cccagacacaac	420
gttgcggacg	tggtaactgtt	gggcgctggc	ttgagccggct	tggagacggc	acgcaaaagtc	480
caggccgcgg	gtctgtcccg	cctcggttctt	gaggcgatgg	atcggtttagg	ggggaaaagact	540
ctgagcgtac	aatcggttcc	cgccgaggacg	actatcaacg	acccctggccgc	tcgggtggatc	600
aatgacagca	acccaaagcga	agtatccaga	ttgtttgaaa	gattttcattt	ggaggggcgag	660
ctccagagga	cgaccggaaa	tccaaatccat	caagcacaac	acggtaacaac	cactacagct	720

<210> 38

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
1				5				10					15		
Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
				20				25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
				35				40					45		
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
				50				55					60		
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65				70					75					80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
				85				90					95		
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
				100				105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
				115				120					125		
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
				130				135					140		
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150				155					160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
					165				170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
					180				185					190	
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
					195				200					205	
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
					210				215					220	
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225					230					235					240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
 260 265 270
 Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 39
 <211> 1930
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1187)

<221> misc_feature
<222> (648) ... (648)
<223> n = A,T,C or G

<400> 39

atggcacttg caccgagctt catcaatccc ccaaaccgtcg cctcccccagg aagggttattct
cacgtcgccg taggccccaga cggaggggagg tatgtgacaa tagctggaca gattggacaa
gacgttccgg ggtgtacaga ccctgcctac gagaaacagg tggcccaagg attcgccaat
ctgcgagctt gcttgcgtgc agtggagcc acttcaaaacgg acgtcaccaa gtcataattac
tacatcgctcg actacgcggcc gagcaaactc accgttaatgg gagatgggtt gaaggctacc
tttgccttgc acaggctccc tcttgcacgg ctgggtgcagg tggccctt gtcgttccat
gaataccctt ttgagggttga tgccaaaggcg ctgggtgcagg gacacacgc cccagacaac
gttgcggacg tggtagtggt gggcgctggc ttgagccgtt tggagacggc acgcaaaatgc
caggccggcg gtcgtgttgc cctcggttgc gggcgatgg atcggtttagg gggaaagact
ctgagcgtaa aatcggttgc cggcaggacg acatatczaacg acctcggtgc tgcgtggatc
aatgacagca accaaaggca agtatacaga ttgtttgaaa gatttcaatnt ggagggcgag
ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct
ccttatgttg actctttggt aagcacaatc ccacitgtg atgagaccc tgcgtgtgt
agaatacagt cactgtatcc acttgcgttca gctgagcgag gaggttgcata gtcgttgc
ggaaactctt cccgtatgtt cttagctgtat cgaagagcat agccttcaag acctcaaggc
gagccctcag gccaaggcgcc tggacagatgtt gagttcgcc cactactgtg agaaggaaact
aaatcggttgc gctgttgc gctgtgttgc aagatccaca cggcgatctgc tgggtgtgg
agcccacggat atcagcatgc ttttttcac cgttacatc aagagtgcctt cccgttccat
taatattttc tcggacaaga aagacggcgcc gcatgtatgtt cgtatgcataa caggtgcgt
tgggtgtgtc tgggtgggg gactcggttgc tcaagtggtc atttcaggta tgcagtcgt
-yuuuayuu alyltcaaaagg aacttgcgttgc aaggctcgttgc cccctccatc cccctgtgc
tgaaatttgag cagtggcat cccgtgttgc agtacgtatgc gcttcggggcc cgggtttccg
aagcaaaaag gtgggtggttt cgttaccggac aaccttgcata cccacccatgc catttttcaacc
acctctccccc gcccggagaagg aagcattggc gggaaatccat atccgtggat actatagca
gatagtcgttgc gtatggaca agccgtggc ggcggaaacaa ggttttcgttgc cggctctccca
atcgagctgt gaccccatct catttgcacgg agataccaggc atcgacgttgc atcgacaaatg
gtcccaatacc tgggttcatgg tggagacccc gggacggaaag tgggttgcaccc agtcccaagg
ggtagcacaat aagtctgtt gggacccact cccgtccatgc tggatggaccc gggggggccca
agtcccaaggcc cccgtccatgc tgctcgaaat cggatgggttgc aagcggcactt atttccaaagg
agtcgttgc gccgttcatgc ggttgcacgg tttcatcaca ctgggttgc gtcgttgc
ggcggttgcagg agtggtttgc tgggttgcaccc gggacggatgtt ttagtttggaa aagggttat
ggaaaggggcc atacgtatgg tgcacccatgc tggatggaccc gttgtggatc gcttgcgttgc
aagcggatcat

<210> 40

<211> 598

<212> PRT

<213> *Exophiala spinifera*

<220>

<221> VARIANT

<222> (216) . . . (216)

<223> Xaa = Any Amino Acid

<400> 40

50	55	60
Leu Ala Ala Val	Gly Ala Thr Ser Asn Asp Val	Thr Lys Leu Asn Tyr
65	70	75
Tyr Ile Val Asp	Tyr Ala Pro Ser Lys Leu Thr Ala Ile	Gly Asp Gly
	85	90
Leu Lys Ala Thr Phe Ala	Leu Asp Arg Leu Pro Pro Cys	Thr Leu Val
100	105	110
Pro Val Ser Ala Leu Ser Ser	Pro Glu Tyr Leu Phe	Glu Val Asp Ala
115	120	125
Thr Ala Leu Val Pro Gly	His Thr Thr Pro Asp Asn Val	Ala Asp Val
130	135	140
Val Val Gly Ala Gly	Leu Ser Gly Leu Glu Thr Ala Arg	Lys Val Gln
145	150	155
Ala Ala Gly Leu Ser Cys	Leu Val Leu Glu Ala Met Asp Arg	Val Gly
165	170	175
Gly Lys Thr Leu Ser Val Gln Ser	Gly Pro Gly Arg Thr Thr	Ile Asn
180	185	190
Asp Leu Gly Ala Ala Trp Ile	Asn Asp Ser Asn Gln Ser	Glu Val Ser
195	200	205
Arg Leu Phe Glu Arg Phe	His Xaa Glu Gly Glu	Leu Gln Arg Thr Thr
210	215	220
Gly Asn Ser Ile His Gln	Ala Gln Asp Gly Thr Thr	Thr Ala Pro
225	230	235
Tyr Gly Asp Ser Leu Leu Ser	Glu Glu Val Ala Ser Ala	Leu Ala Glu
245	250	255
Leu Leu Pro Val Trp Ser Gln	Leu Ile Glu Glu His Ser	Leu Gln Asp
260	265	270
Leu Lys Ala Ser Pro Gln	Ala Lys Arg Leu Asp Ser	Val Ser Phe Ala
275	280	285
His Tyr Cys Glu Lys Glu	Leu Asn Leu Pro Ala Val	Leu Gly Val Asn
290	295	300
Gln Ile Thr Arg Ala Leu	Leu Gly Val Ala His Glu Ile Ser	Met
305	310	315
Leu Phe Leu Thr Asp Tyr	Ile Lys Ser Ala Thr Gly	Leu Ser Asn Ile
325	330	335
Phe Ser Asp Lys Lys Asp	Gly Gln Tyr Met Arg Cys	Lys Thr Gly
340	345	350
Met Gln Ser Ile Cys His	Ala Met Ser Lys Glu	Leu Val Pro Gly Ser
355	360	365
Val His Leu Asn Thr Pro	Val Ala Glu Ile Glu	Gln Ser Ala Ser Gly
370	375	380
Cys Thr Val Arg Ser Ala	Ser Gly Ala Val Phe	Arg Ser Lys Val
385	390	395
Val Val Ser Leu Pro Thr	Thr Leu Tyr Pro Thr	Leu Thr Phe Ser Pro
405	410	415
Pro Leu Pro Ala Glu Lys	Gln Ala Leu Ala Glu Asn	Ser Ile Leu Gly
420	425	430
Tyr Tyr Ser Lys Ile Val	Phe Val Trp Asp Lys	Pro Trp Trp Arg Glu
435	440	445
Gln Gly Phe Ser Gly Val	Leu Gln Ser Ser Cys	Asp Pro Ile Ser Phe
450	455	460
Ala Arg Asp Thr Ser Ile	Asp Val Asp Arg Gln	Trp Ser Ile Thr Cys
465	470	475
Phe Met Val Gly Asp Pro	Gly Arg Lys Trp Ser	Gln Gln Ser Lys Gln
485	490	495
Val Arg Gln Lys Ser Val	Trp Asp Gln Leu Arg	Ala Ala Tyr Glu Asn
500	505	510
Ala Gly Ala Gln Val	Pro Glu Pro Ala Asn	Val Leu Glu Ile Glu Trp

515	520	525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu		
530	535	540
Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser		
545	550	555
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met		
565	570	575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala		
580	585	590
Ser Leu Val Pro Ala Ala		
595		

<210> 41
 <211> 1928
 <212> DNA
 <213> Rhinocladiella atrovirens

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1185)

<400> 41

atggcacttg	caccgagcta	catcaatccc	ccaaacacctcg	cctcccccagc	agggtatcc	60
cacgtccggcg	taggccccaaa	cggaaggagg	tatgcgacaa	taatggacaca	gatgggacaa	120
gacgttccgg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgcccaagc	attcgccaaac	180
ctgcgagtt	gtcttgcgtc	agttggagcc	acttcazaacg	acattaccaa	gtcaattac	240
tacatcgtcg	actacaaccc	gagcaaactc	accgcaattg	gagatgggt	gaaggctacc	300
tttgccttg	acaggctccc	tccttgcacg	ctgggtgcag	tgccggccct	ggcttcaccc	360
gaatacccc	ttgaggttga	tgccacggcg	ctgggtccag	gacactcaac	cccagacaat	420
gttgccgacg	tggtcggtt	gggcgcgtggc	ttgagcggtt	tggagacggc	acgcaaagtc	480
caggctgccc	ggctgttcgt	cctcgttctt	gaggcgatgg	atcggtgtgg	gggaaagact	540
ctgagcgtac	aatcggttcc	cggcaggacg	gtatcaatg	accccgccgc	tgcgtggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcyaag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatggtg	atcccccttgt	aagcacaatt	ccatcttgc	atgagacetc	tgtcggttgt	780
agaatacagt	cgctgacccc	acatcgtc	gtcgagcgag	gagggtgc	gtgcactcgc	840
ggaactccct	cccgcatttgt	ctcagctgt	cgaaagagcat	agtcttgc	accccaaggc	900
gagccctcaa	gcgaaggcgc	tcgacagtgt	gagcttcgca	cactactgt	agaaggatct	960
aagcttgcct	gtctgttcgt	gctgtggccaa	ccagatcaca	cgcgctctgc	tgcgtgtgg	1020
agcccacgag	atcagcattgc	tttttctc	cgactacatc	aagatgtcc	ccggctctca	1080
taatatttgc	tcggataaga	aagacggtgg	gcagttat	cgatgc	aaaaaa	1140
tggtgttctc	tcagtggttgc	actcgtttct	tagtggcat	tccagtgat	cgatcgcttt	1200
gcccaaggccat	gtccaaaggaa	tttgcgtccag	gtctcgtgc	cctcaacacc	cccgctccgc	1260
aaatttgc	gtcggtatcc	ggctgtacag	tacgatccgc	ctcgccgg	gtgttccgaa	1320
gtaaaaagggt	gtgtgtttcg	ttaccgacaa	cttgcattcc	ccacttgata	ttttcaccac	1380
ctcttccgc	cgagaaggcaa	gtatggctg	aaaaatccat	ctgggtctac	taatagcaaga	1440
tagtcttgc	atgggacaag	ccgtgttggc	gcgaacaagg	cttcgtggc	gtcttccaaat	1500
cgagctgtga	ccccatctca	tttgcctagag	ataccagcat	cgaagtcgt	cggtcaatgg	1560
ccattacctg	tttcatggtc	ggagacccgg	gacggaaatgc	gtcccaacag	tccaaagcagg	1620
tacgacagaa	gtctgttgc	aaccaactcc	cgccagccct	cgagaacgc	ggggcccaag	1680
tcccaaggcc	ggccaaacgt	ctcgagatcg	agtgggtcgaa	gcagcaatgt	ttccaaaggag	1740
cgcccgacgt	cgcttatggg	ctgaactgtc	tcaacacact	gggttccggcg	ctcagaacgc	1800
cgttcaagggg	tgttcat	gttggaaacgg	agacgtcttt	gttttggaaa	gggtatatgg	1860
aggggccat	atcgatcggt	cagcgaggcg	ctgcagaaatgt	tgtgggttgc	ttggtgcac	1920
cagcatag						1928

<210> 42
 <211> 598
 <212> PRT
 <213> Rhinocladiella atrovirens

<400> 42

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gin Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
 210 215 220
 Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
 225 230 235 240
 Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
 245 250 255
 Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
 260 265 270
 Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
 275 280 285
 Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
 290 295 300
 Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
 305 310 315 320
 Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
 325 330 335
 Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
 340 345 350
 Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
 355 360 365
 Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
 370 375 380
 Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
 385 390 395 400
 Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro

405	410	415
Pro Leu Pro Ala Glu Lys Gln Ala	Leu Ala Glu Lys Ser Ile Leu Gly	
420	425	430
Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu		
435	440	445
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe		
450	455	460
Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys		
465	470	475
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln		
485	490	495
Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn		
500	505	510
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp		
515	520	525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu		
530	535	540
Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly		
545	550	555
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met		
565	570	575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala		
580	585	590
Ser Leu Val Pro Ala Ala		
595		

<210> 43
 <211> 1928
 <212> DNA
 <213> Rhinocladiella atrovirens

<220>
 <221> intron
 <222> (739)....(811)

 <221> intron
 <222> (1134)....(1186)

<400> 43

atggcacttg	caccgagct	catcaatccc	ccaaacctcg	cctcccccagc	agggtattcc	60
tacgtcgccg	taggccccaa	cgaggggagg	tatgtaccaa	tagctggaca	gattggacaa	120
gacgttccgg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgcccaga	atcgccaaac	180
ctgcgcgg	gtcttgcgtc	agtgggagcc	acttcaaaacg	acattaccaa	gtcaattac	240
tacatcgctc	actacaaccc	gagcaaaactc	accgcaattt	gagatgggt	gaaggctacc	300
tttgccttgc	acaggctccc	tccttgcacg	ctgggtgcag	tgccggccct	ggttcacct	360
gaataccctt	ttgaggttga	tgccacggcg	ctgggttccag	gacactcaac	ccagacaaat	420
gttgcggacc	tggtcgttgt	gggcgcgtggc	ttggnggggt	tggagacgge	acgcggaaagtc	480
caggtgcgg	ggctgttctg	cctcggttctt	gaggcgatgg	atcggtgggg	ggaaagagact	540
ctgagcgatc	aatcggttcc	cggcaggacg	actatcaatg	acctcgccgc	tgcgtggatc	600
aatgacagca	acccaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
cgtccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaaac	cactacagct	720
ccttatggtg	attcccttgt	aagcacaatt	ccatcttgcgt	atgagacactc	tgtcggtgt	780
agaatatacg	cgctgactcc	acatcgccca	gtcgacgtgg	gagggttgcac	gtgcactcgcc	840
ggaaactccctt	cccgcatgtt	ctcagctgtat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	cgcaaggcgc	tcgacagtgt	gagcttcgcac	cactactgtg	agaaggaaatc	960
aaaccttgcct	gtgtttctcg	cggtggccaaa	ccagatcaca	cgcgctctgc	tcgggtgtgg	1020
agcccaacggg	atcgacatgt	cttttctcact	cgactacatc	aaagatgcac	ccgggtctcag	1080
taatattgtc	tcggataaga	aagacgggg	cgagtatatg	cgatgcaaaa	ccgggtcgctg	1140

tgggttttc tcagtggag acttgttct tagtgtcat tccaggtatg cagtcgtttt 1200
 gccatgccat gtcaaaggaa cttgttccag gtcagtgca cctcaacacc cccgtcgccg 1260
 aaartgagca gtcggcattcc ggctgtacag taacgatggc ctcggggcgc gtgtttccgaa 1320
 gtaaaaaagggt gtttttttcc ttaccqacaa ccttgtatcc cacctgata tttttcaccat 1380
 ctcttcccgc cgagaagcaa gcattggctg aaaaatccat cctgggtatc tatagcaaga 1440
 tagtttctgt atgggacaaag cctgggtggc gogaacaagg ctttcgggc gtccicccat 1500
 cgagctgtga ccccatctca tttggccagaa ataccagcat cgaagtcgtat cggcaatgg 1560
 ccattacctg ttttcatggc ggagacccgg cacggaaagt gtcggcaacag tccaaaggc 1620
 taacgacagaa gtcgtgttgg aaccaactcc ggcgcagectca cgagaacggc gggggcccaag 1680
 tccagagaccc ggcggcaacgtg ctggagatcg agtggtagaa gcaagcgtat tttccaggaa 1740
 cggcggcgc cgtctatggc ctgaactgtc tcaacacact gggttcggcg ctcaacacgc 1800
 cgttcaagggg tggttcatttc gttggaaacgg agacgtttt ggtttggaaa ggttatatgg 1860
 aaggggccat acgatcgggt cagcggcgc ctgcagaagt tgggtctagc ctggtgccag 1920
 cagcatag 1928

<210> 44

<211> 591

<212> PRT

<213> Rhinocladiella atrovirens

<400> 44

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
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 Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
 180 185 190
 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
 195 200 205
 Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
 210 215 220
 Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
 225 230 235 240
 Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
 245 250 255
 Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
 260 265 270
 Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 275 280 285
 Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg

290	295	300
Ala	Leu	Leu
Gly	Val	Glu
Ala	His	Ile
Glu	Ile	Ser
Met	Phe	Phe
Leu	Thr	
305	310	315
Asp	Tyr	Ile
Lys	Ser	Ala
Thr	Gly	Leu
Ser	Asn	Ile
Asp	Asp	Val
Lys		Ser
Asp	Gly	Gly
Gln	Tyr	Met
Arg	Cys	Gly
Lys	Thr	Met
Cys		Gln
His	Ala	Ser
Met	Ser	Lys
Glu	Leu	Val
Pro	Cly	Ser
Val	His	Leu
Asn		
355	360	365
Thr	Pro	Val
Ala	Glu	Ile
Glu	Gln	Ser
Ala	Ser	Gly
Cys		
Thr	Val	Arg
370	375	380
Ser	Ala	Ser
Gly	Gly	Val
Phe	Arg	Ser
Lys	Lys	Val
Val	Val	Leu
Pro		Pro
385	390	395
Leu	Tyr	Pro
Thr	Leu	Ile
Phe	Ser	Pro
Pro	Ile	Pro
Ala	Glu	Lys
Gln		
405	410	415
Ala	Leu	Ala
Glu	Lys	Ser
Ile	Leu	Gly
Tyr	Tyr	Ser
Lys	Ile	Val
Phe		
420	425	430
Val	Trp	Asp
Lys	Pro	Trp
Trp	Arg	Glu
Gln	Gly	Phe
Ser		Ser
435	440	445
Gln	Ser	Cys
Asp	Asp	Pro
Ile	Ser	Phe
Ala	Arg	Asp
Asp	Thr	Ser
Ile		
450	455	460
Val	Asp	Arg
Gln	Trp	Ser
Ile	Thr	Cys
Phe	Met	Val
Gly		
465	470	475
Arg	Lys	Trp
Ser	Gln	Ser
Lys	Gln	Val
Arg		
485	490	495
Asn	Gln	Leu
Leu	Arg	Ala
Ala	Ala	Tyr
Glu	Asn	Ala
Ala	Gly	Gly
Gly		
500	505	510
Pro	Ala	Asn
Asn	Val	Leu
Glu	Ile	Glu
Trp	Ser	Lys
Gln	Gln	Tyr
Tyr		
515	520	525
Gly	Ala	Pro
Ala	Ser	Ala
Val	Tyr	Gly
Leu	Asn	Cys
Ile	Asn	Thr
Gly		
530	535	540
Ser	Ala	Leu
Leu	Arg	Thr
Thr	Pro	Phe
Lys	Gly	Val
His	Phe	Gly
545	550	555
Thr	Ser	Leu
Leu	Val	Trp
Iys	Gly	Tyr
Met	Glu	Gly
Ala	Ile	Arg
Ile	Arg	Ser
Gly		
565	570	575
Gln	Arg	Gly
Ala	Ala	Glu
Glu	Val	Val
Ala	Ser	Leu
Ala	Val	Pro
Ala		
580	585	590

<210> 45

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

<220>

<221> intron

<222> (739)...(811)

<221> intron

<222> (1134)...(1185) .

<400> 45

atggcact	g caccgagct	ta	catcaat	ccc	ccaa	ac	tcg	cct	ccc	agg	gt	att	cc	60
tcg	cg	cg	cg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	120
cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	180
cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	240
cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	300
cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	360
cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	420

gttgtggacg	tggtgtgtgt	gssgtggc	tttggatggc	tggagacggc	acgcaasgtc	420
caggctggcg	ggctgtcccg	cctcgttctt	gaggcgatgg	atcggtgtgg	gggaaagact	540
ctgagcgta	aatcggtcc	cggtggacg	actataatg	acctcggcgc	tgcgtggatc	600
aatgacagca	acccaaagcga	agtattcaaa	ttatgtgaaa	gatttcaatt	ggagggcgag	660
ctccagagga	cgacccggaaa	ttcaatccat	caagcacaag	acggtacaat	cactacagct	720
ccttatggtg	atccccgtgt	aggcacaatt	ccatcttgc	atgagacctc	tgtcgtgtgt	780
agaatracagt	cgtgactcc	acatcgtcca	gctgagcgag	gaggtgtgca	gtgcactcg	840
gaaactccct	cccgcgtgt	ctcagctgtat	cgaaagagcat	agtctgtgaa	accccaagcc	900
gagccctcaa	gccaaggcgc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aaacttgcct	gtctgtctcg	gctgtggcaaa	ccagatcaca	cgccgcgtgc	tgcgtgtgca	1020
agcccaacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgc	ccgggtctca	1080
taatattgtc	tcggataaga	aagacggtgg	gcaatataatg	cgatgc	aaaaaaggatc	1140
tggtgttctc	tcagttggag	actcgtttct	taatgtgtcat	tccaggtatg	cagtcgctt	1200
gccatggccat	gtccaaaggaa	cttggccag	gtctcgtgtca	cctcaacacc	cccggtggcc	1260
aaatttgcgt	gtcggtatcc	ggctgtacag	tacgtcgcc	ctcggtggcc	gtgttccgaa	1320
gtaaaaaggt	gggtgttcc	ttacccgacaa	cttgcgtatcc	cacctgtata	ttttcaccac	1380
ctcttccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ctgtgggtggc	gcgaacaagg	cctctccggc	gtctccaaat	1500
cgagctgtga	ccccatctca	tttgcctagag	ataccagcat	cgaagtcgt	ggcaatgg	1560
ccattacctg	tttcauggtc	ggagccccgg	gacggaaatg	gtcccaacag	cccaaggcagg	1620
taacacagaa	gtctgtctgg	aaccaactcc	gcgcagccca	cgagaacgc	ggggcccaag	1680
tccctagagcc	ggccaaacgtg	ctcgagatcg	agtgggtcgaa	gcagcgtat	cccaaggag	1740
cgccggcgcc	cgtctatgg	ctgaactgtc	tcaacacat	gggttccggc	ctcagaacgc	1800
cgttcaaggg	tgttcatitc	gttggaaacgg	agacgtctt	gttggaaa	gggttatatgg	1860
aaggggccat	acgtatgggt	cagcgaggcg	ctgcagaagt	tgtgcctagc	cggggccag	1920
cacatag						1928

<210> 46

<211> 591

<212> PRT

<213> Rhinocladiella atrovirens

<400> 46

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Ala	Ser	Pro	Ala
1							5				10				15
Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val	Thr
							20				25				30
Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro	Ala
							35				40				45
Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	Leu
							50				55				60
Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr	Tyr
							65				70				75
Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	Leu
							85				90				95
Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	Pro
							100				105				110
Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	Thr
							115				120				125
Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	Val
							130				135				140
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
							145				150				155
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
							165				170				175
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
							180				185				190
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Phe
															80

195	200	205
Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr		
210	215	220
Gly Asn Ser Ile His His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro		
225	230	235
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu		
245	250	255
Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp		
260	265	270
Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala		
275	280	285
His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala		
290	295	300
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser		
305	310	315
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn		
325	330	335
Ile Val Ser Asp Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr		
340	345	350
Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly		
355	360	365
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser		
370	375	380
Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys		
385	390	395
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu		
405	410	415
Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser		
420	425	430
Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser		
435	440	445
Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr		
450	455	460
Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp		
465	470	475
Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val		
485	490	495
Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro		
500	505	510
Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe		
515	520	525
Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly		
530	535	540
Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu		
545	550	555
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly		
565	570	575
Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala		
580	585	590

<210> 47

<211> 600

<212> PRT

<213> Exophiala spinifera

<400> 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro		
1	5	10

15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
 260 265 270
 Asp Leu Lys Ala Ser Pro Cln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Phe Ser Asp Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
 465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Gln Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 48
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 48

aaa gac aac gtt gct gac gtc gta gtc gtc ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gct ctg tcc tgc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

gac ggt aca acc act aca gct ttt ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110

gag gtt gca agt gca ctt gct gaa ctc ctc ccc gta tgg ttt cag ctg 384
 83

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag			432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac			480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
tgt cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc			528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc			576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc			624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc			672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgc aca gta cga tcg gcc tcg			768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc			816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa			864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc			912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc			960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc agt gat acc agc atc gac			1008
Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga			1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc eac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1346
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	
<210> 49	
<211> 463	
<212> PRT	
<213> Unknown	
<220>	
<223> Cys (-) APAO; removal of cysteine 461	
<400> 49	
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
85	

145	150	155	160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
Arg Lys Trp Ser Gln Cln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	

<210> 50
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50

aaa gac aac gtt gcg gac gtc gta gtc gtc ggc gct ggc ttg agc ggt	48		
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly			
1	5	10	15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt cag tcc tgc ctc gtc	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	

20	25	30	
cct gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Ile Ser Val Gln Ser			144
35	40	45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			192
50	55	60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ctg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			240
55	70	75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			288
85	90	95	
gac ggt aca acc act aca gct ctt tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			336
100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			384
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc ctt cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			432
130	135	140	
ccg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			480
145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			528
165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			576
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			624
195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala			672
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			720
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			768
245	250	255	

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccc aca acc	815
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca oct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Ieu Thr Phe Ser Pro Pro Ieu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccc tgg cgc gaa caa gcc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttc gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgg ttc atg gtc gga gac ccc gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1295
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 51
 <211> 463
 <212> PRT
 <213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Gln
 420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 52

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 52

aaa gac aac gtt gcg gac gtc gta gtc gtc gtc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Gln
 100 105 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag 432
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140

ccg ctc gac agt gtc agc ttc gcg cac tac tgt gag aag gaa cta aac 480
 Arg Leu Asp Ser Val Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctc Leu Pro Ala Val Ieu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175	528
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190	576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205	624
ggc cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220	672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255	768
ggc gcc ctc cga agc aaa aag gtc gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
ccg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	1200

385	390	395	400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly				1248
405		410	415	
tcc gcc ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu				1296
420	425	430		
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly				1344
435	440	445		
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *				1392
450	455	460		
 <210> 53				
<211> 463				
<212> PRT				
<213> Unknown				
 <220>				
<223> Cys (-) APAC; removal of cysteines 169, 359, and				
461				
 <400> 53				
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly				
1	5	10	15	
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val				
20		25	30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				
35	40	45		
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				
50	55	60		
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				
65	70	75	80	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				
85		90	95	
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				
100	105	110		
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
115	120	125		
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
130	135	140		
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
145	150	155	160	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu				
165		170	175	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile				
180	185	190		
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly				
195	200	205		
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala				
210	215	220		
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val				
92				

225	230	235	240
Ala Glu Ile Glu Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	

<210> 54
 <211> 8
 <212> PRT
 <213> Unknown

 <220>
 <223> Artificial Sequence

 <400> 54

Gly Gly Gly Ser Gly Gly Gly Ser
 1 5

<210> 55
 <211> 11
 <212> PRT
 <213> Exophilal spinifera

 <400> 55

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10